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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=3; day=20; hr=17; min=21; sec=17; ms=821; ]

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\*\*\*\*\*

Reviewer Comments:

<400> 696

Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly
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Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			20					25					30		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln
		35					40					45			
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	50					55					60				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr
	65				70					75				80	
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Xaa
			85						90					95	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Xaa	Lys	Gly	Leu	Pro	Ser	Ser
			100					105					110		
Ile	Glu	Lys	Thr	Ile	Ser	Xaa	Ala	Xaa	Gly	Gln	Pro	Arg	Glu	Pro	Gln
		115					120						125		

Per the above sequence id# 696, please explain "Xaa" at locations 96, 106, 119 and 121. Please check the remaining sequences for similar errors.

\*\*\*\*\*

Application No: 10566409 Version No: 1.0

Input Set:

Output Set:

Started: 2009-02-26 18:37:15.342  
Finished: 2009-02-26 18:37:59.763  
Elapsed: 0 hr(s) 0 min(s) 44 sec(s) 421 ms  
Total Warnings: 631  
Total Errors: 13  
No. of SeqIDs Defined: 699  
Actual SeqID Count: 699

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)

**Input Set:**

**Output Set:**

**Started:** 2009-02-26 18:37:15.342  
**Finished:** 2009-02-26 18:37:59.763  
**Elapsed:** 0 hr(s) 0 min(s) 44 sec(s) 421 ms  
**Total Warnings:** 631  
**Total Errors:** 13  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (201)
W 402	Undefined organism found in <213> in SEQ ID (202)
W 402	Undefined organism found in <213> in SEQ ID (203)
W 402	Undefined organism found in <213> in SEQ ID (204)
W 402	Undefined organism found in <213> in SEQ ID (205)
W 402	Undefined organism found in <213> in SEQ ID (206)
E 257	Invalid sequence data feature in <221> in SEQ ID (212)
E 257	Invalid sequence data feature in <221> in SEQ ID (216)
W 402	Undefined organism found in <213> in SEQ ID (451)
W 402	Undefined organism found in <213> in SEQ ID (452)
W 402	Undefined organism found in <213> in SEQ ID (457)
W 402	Undefined organism found in <213> in SEQ ID (458)
W 251	Found intentionally skipped sequence in SEQID (520 )
W 251	Found intentionally skipped sequence in SEQID (521 )
W 251	Found intentionally skipped sequence in SEQID (522 )
W 251	Found intentionally skipped sequence in SEQID (523 )
W 251	Found intentionally skipped sequence in SEQID (524 )
W 251	Found intentionally skipped sequence in SEQID (525 )
W 251	Found intentionally skipped sequence in SEQID (526 )
W 251	Found intentionally skipped sequence in SEQID (527 )
W 251	Found intentionally skipped sequence in SEQID (639 )

**Input Set:**

**Output Set:**

**Started:** 2009-02-26 18:37:15.342  
**Finished:** 2009-02-26 18:37:59.763  
**Elapsed:** 0 hr(s) 0 min(s) 44 sec(s) 421 ms  
**Total Warnings:** 631  
**Total Errors:** 13  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (640 )
W 251	Found intentionally skipped sequence in SEQID (643 )
W 251	Found intentionally skipped sequence in SEQID (646 )
W 251	Found intentionally skipped sequence in SEQID (680 )
W 251	Found intentionally skipped sequence in SEQID (681 )
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
W 251	Found intentionally skipped sequence in SEQID (688 )
W 251	Found intentionally skipped sequence in SEQID (689 )
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 341	'Xaa' position not defined SEQID (696) POS (96)
E 341	'Xaa' position not defined SEQID (696) POS (106)
E 341	'Xaa' position not defined SEQID (696) POS (119)
E 341	'Xaa' position not defined SEQID (696) POS (121)
W 251	Found intentionally skipped sequence in SEQID (699 )

<110> Ledbetter, Jeffrey A.  
Hayden-Ledbetter, Martha S.  
Thompson, Peter A.

<120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.40102USPC

<140> 10566409

<141> 2009-02-26

<150> PCT/US2003/041600

<151> 2003-12-24

<150> US 10/627,556

<151> 2003-07-26

<150> US 10/053,530

<151> 2002-01-17

<150> US 60/367,358

<151> 2001-01-17

<160> 699

<170> PatentIn version 3.2

<210> 1

<211> 714

<212> DNA

<213> Homo sapiens

<400> 1

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atctcccgga	cccctgaggt	cacatgcgtg	gtggtggacg	tgagccacga	agaccctgag	180
gtcaagtcca	actgttacgt	ggacggcggtg	gaggtgcata	atgccaaagac	aaagccgcgg	240
gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	300
tggtgtaatg	gcaaggagta	caagtgcaag	gtctccaaca	aagccctccc	agcccccatc	360
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ccatccccggg	atgagctgac	caagaaccag	gtcagcctga	cctgcctggg	caaaggcttc	480
tatcccagcg	acatcgccgt	ggagtgggag	agcaatgggc	agccggagaa	caactacaag	540
accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	gtcaccgtg	600
gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggetctg	660
cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtaaatgatc	taga	714

<210> 2

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2

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Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
				20				25					30		
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				35			40						45		

Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
50						55					60				
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
65					70					75					80
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
				85					90					95	
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
			100					105					110		
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
		115					120						125		
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
		130					135						140		
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
145					150					155					160
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
				165					170						175
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
			180					185						190	
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
		195					200						205		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
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Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
225					230					235					

<210> 3

<211> 718

<212> DNA

<213> Lama glama

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<222> (34)..(34)

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<222> (52)..(52)

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<221> modified\_base

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ttttggaggc	cgagtcacgt	gcgtttagt	ggacgtcgga	aagaaagacc	ccgaggtcaa	180

tttcaactgg	tatattgatg	gcggttgaggt	gcgaacggcc	aatacgaagc	caaaagagga	240
acagttcaac	agcacgtacc	gcggtggtcag	cgtcctgccc	atccagcacc	aggactggct	300
gacggggaag	gaattcaagt	gcaaggtcaa	caacaaagct	ctcccggccc	ccatcgagag	360
gaccatctcc	aaggccaaag	ggcagacccg	ggagccgcag	gtgtacaccc	tggccccaca	420
ccgggaagaa	ctggccaagg	acaccgtgag	cgtaacatgc	ctgggtcaaag	gcttctaccc	480
agctgacatc	aacgttgagt	ggcagaggaa	cggtcagccg	gagtcagagg	gcacctacgc	540
caacacgccg	ccacagctgg	acaacgacgg	gacctacttc	ctctacagca	agctctcggt	600
gggaaagaac	acgtggcagc	ggggagaaac	cttaacctgt	gtggtgatgc	atgaggccct	660
gcacaaccac	tacaccagca	aatccatcac	ccagtcttcg	ggtaaatagt	aatctaga	718

<210> 4

<211> 231

<212> PRT

<213> Lama glama

<400> 4

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Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
			20					25					30		
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		35					40					45			
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
50						55					60				
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Gln	Phe	Asn	Ser	
65					70					75				80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
				85					90					95	
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
			100						105				110		
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
		115					120					125			
Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr
130						135					140				
Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ala	Asp	Ile	Asn
145					150					155					160
Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala
			165						170					175	
Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser
			180						185				190		
Arg	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Arg	Gly	Glu	Thr	Leu	Thr
	195					200					205				
Gly	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
210						215					220				
Ile	Thr	Gln	Ser	Ser	Gly	Lys									
225					230										

<210> 5

<211> 757

<212> DNA

<213> Lama glama

<400> 5

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catcttcccc	ccgaaccca	aggacgtcct	ctccatttct	gggaggcccg	aggtcacgtg	180
cgttgtggta	gacgtgggcc	aggaagaccc	cgaggctcagt	ttcaactggg	acattgatgg	240
cgctgaggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgtaccg	300
cgtggtcagc	gtcctgcccc	tccagcacca	ggactggctg	acggggaagg	aattcaagtg	360

caaggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagaccggg	gagccgcagg	tgtacaccct	ggccccacac	cgggaagagc	tgccaagga	480
caccgtgagc	gtaacatgcc	tgggtcaaagg	cttctacceca	cctgatataca	acgttgagtg	540
gcagaggaat	gggcagccgg	agtcagaggg	cacytacgcc	accacgccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcgggtg	ggaaagaaca	cgtggcagca	660
gggagaaacc	ttcacctgtg	tgggtgatgca	cgaggccctg	cacaaccact	acacccagaa	720
atccatcacc	cagtcttcgg	gtaaatagta	atctaga			757

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<211> 248

<212> PRT

<213> Lama glama

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			20					25				30			
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp
		35					40					45			
Val	Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
	50					55					60				
Val	Gly	Gln	Glu	Asp	Pro	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	Asp	Gly
65					70					75				80	
Ala	Glu	Val	Arg	Thr	Ala	Asn	Thr	Arg	Pro	Lys	Glu	Glu	Gln	Phe	Asn
				85				90						95	
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp
			100					105					110		
Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro
		115					120					125			
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu
	130					135					140				
Pro	Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp
145					150					155				160	
Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	Asp	Ile
			165					170						175	
Asn	Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr
		180					185						190		
Ala	Thr	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr
		195				200						205			
Ser	Lys	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Gln	Gly	Glu	Thr	Phe
	210					215					220				
Thr	Cys	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
225					230					235				240	
Ser	Ile	Thr	Gln	Ser	Ser	Gly	Lys								
					245										

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<211> 727

<212> DNA

<213> Lama glama

<400> 7

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cacccgaaaa	cctgaggtca	cgtgcttggtg	gtggacgtgg	gtaaagaaga	ccctgagatc	180
gagttcaagc	tggtccgtgg	atgacacaga	ggtacacacg	gctgagacaa	agccaaagga	240
ggaacagttc	aacagcacgt	accgcgtggt	cagcgtcctg	cccatccagc	accaggactg	300
gctgacgggg	aaggaattca	agtgcaaggt	caacaacaaa	gctctcccag	cccccatcga	360



gaggaccatc	tccaaggcca	aagggcagac	ccgggagccg	caggtgtaca	ccctggcccc	420
acaccgggaa	gagctggcca	aggacaccgt	gagcgtaacc	tgcttggtca	aaggcttctt	480
cccagctgac	atcaacgttg	agtggcagag	gaatgggcag	ccggagtcag	agggcaccta	540
cgccaacacg	ccgccacagc	tggaacaacga	cgggacctac	ttcctctaca	gcaaactctc	600
cgtgggaaag	aacacgtggc	agcagggaga	agtcttcacc	tgtgtggtga	tgacagagggc	660
tctacacaat	cactccaccc	agaaatccat	caccagctct	tcgggtaaat	agtaatctag	720
agggcc						727

<210> 8

<211> 236

<212> PRT

<213> Lama glama

<400> 8

Asp	Gln	Ala	His	His	Ser	Glu	Asp	Pro	Ser	Ser	Lys	Cys	Pro	Lys	Cys
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Pro	Gly	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Thr	Val	Phe	Ile	Phe	Pro	Pro
			20					25					30		
Lys	Ala	Lys	Asp	Val	Leu	Ser	Ile	Thr	Arg	Lys	Pro	Glu	Val	Thr	Cys
			35				40						45		
Leu	Trp	Trp	Thr	Trp	Val	Lys	Lys	Thr	Leu	Arg	Ser	Ser	Ser	Ser	Trp
	50					55					60				
Ser	Val	Asp	Asp	Thr	Glu	Val	His	Thr	Ala	Glu	Thr	Lys	Pro	Lys	Glu
65					70					75				80	
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln
			85					90						95	
His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn
			100					105					110		
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly
			115				120						125		
Gln	Thr	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu
	130					135					140				
Leu	Ala	Lys	Asp	Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Phe
145					150					155				160	
Pro	Ala	Asp	Ile	Asn	Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser
				165				170						175	
Glu	Gly	Thr	Tyr	Ala	Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr
			180					185					190		
Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Gln
	195					200							205		
Gly	Glu	Val	Phe	Thr	Cys	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His
	210					215					220				
Ser	Thr	Gln	Lys	Ser	Ile	Thr	Gln	Ser	Ser	Gly	Lys				
225					230					235					

<210> 9

<211> 54

<212> DNA

<213> Homo sapiens

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<210> 10

<211> 18

<212> PRT

<213> Homo sapiens

<400> 10

Asp	Gln	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
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1              5              10              15
Pro Ala

<210> 11
<211> 54
<212> DNA
<213> Homo sapiens
<400> 11
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<210> 12
<211> 18
<212> PRT
<213> Homo sapiens
<400> 12
Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1              5              10              15
Pro Ala

<210> 13
<211> 327
<212> DNA
<213> Homo sapiens
<400> 13
cctgaactcc tgggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc      60
atgatctccc ggacccttga ggtcacatgc gtgggtggtg acgtgagcca cgaagaccct      120
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg      180
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag      240
gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagccccc      300
atcgagaaaa ccattctcaa agccaaa      327

<210> 14
<211> 109
<212> PRT
<213> Homo sapiens
<400> 14
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1              5              10              15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20              25              30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
35              40              45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50              55              60
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65              70              75              80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
85              90              95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100             105

<210> 15
<211> 324
<212> DNA
<213> Homo sapiens
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 180
gacggctcct tcttctctta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240
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ctctccctgt ccccggttaa atga 324

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<210> 16  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 <400> 16

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Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
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Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
          20          25          30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
          35          40          45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
          50          55          60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65          70          75          80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
          85          90          95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
          100          105

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<210> 17  
 <211> 54  
 <212> DNA  
 <213> Homo sapiens  
 <400> 17

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<210> 18  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens  
 <400> 18

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Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
1          5          10          15
Pro Ala

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<210> 19  
 <211> 712  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Synthetic  
 nucleotide sequence  
 <400> 19

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tgatcacccc aaattctctg acaaaaactca cacatctcca ccgtctctcag cacctgaact 60
cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc 120
ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa 180
gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga 240

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